AMENDMENTS TO THE SPECIFICATION

Please delete the sequence listing from the international application and replace it with the sequence listing submitted on compact disc enclosed herewith.

In the specification at page 1, after the title and before line 3, please insert the following:

RELATED APPLICATIONS

This application is a national stage application (under 35 U.S.C. 371) of PCT/EP2004/011294 filed October 8, 2004 which claims benefit to European application 03022783.9 filed October 10, 2003 and European application 04007051.8 filed March 24, 2003.

INCORPORATION OF SEQUENCE LISTING

The contents of the following submission on compact discs are incorporated herein by reference in its entirety: two copies of the Sequence Listing (COPY 1 and COPY 2) and a computer-readable form of the Sequence Listing (CRF COPY), all on CD-ROMs, each containing: file name: Final Sequence list-13987-00003-US, date recorded: April 6, 2006, size: 131 KB.

In the specification at page 5 line 10, please replace the paragraph starting with "Degenerate primers" with the following amended paragraph:

Degenerate primers were designed according to these peptides (see example 4) and used for PCR with cDNA as template. A 837 bp fragment was amplified with the following primers: 5'-GGITGGTAYAAYACIGTIGC-3' (SEQ ID NO: 12) (referring to peptide 7) and 5'-GTYTCRTAICCIGCRAARTC-3' (SEQ ID NO: 13) (referring to peptide 9). This fragment was cloned into pBluescript SK+/HincII and sequenced (SEQ ID NO : 3). The translated sequence contained several peptides of the purified protein and therefore the 837 bp fragment was used as hybridisation probe to screen a cDNA library constructed with mRNA from Euglena cells. Screening of 250.000 recombinant phages resulted in six independent clones. cDNA inserts varied between 1600 bp and 1900 bp. Sequencing of all six clones from both ends revealed that

all clones represented the same transcript and varied only in length. The longest clone was sequenced completely double-stranded via deletion by exonuclease III. The clone had a length of 1912 bp and encodes an open reading frame of 1620 bp coding for 539 aa (SEQ ID NO : 1 and SEQ ID NO : 2). At both ends it had adaptors consisting of a NotI and EcoRI restriction site and was inserted into the EcoRI site of the vector pBluescript SK+, see figure 3.

In the specification at page 18 line 17, please replace the paragraph starting with "Table 3 shows" with the following amended paragraph:

Table 3 shows the amino acid sequence of TER (SEQ ID NO: 2) compared to the amino acid sequence of these homologous nucleic acids (Q88E33 (SEQ ID NO: 35), Q8D795 (SEQ ID NO: 36), Q8D8Y6 (SEQ ID NO: 37), Q8EG14 (SEQ ID NO: 38), Q8PE66 (SEQ ID NO: 39), Q8PR25 (SEQ ID NO: 40), Q8XIP1 (SEQ ID NO: 41), Q93HE4 (SEQ ID NO: 42), A83277 (SEQ ID NO: 43), AD0498 (SEQ ID NO: 44), B82164 (SEQ ID NO: 45), B82418 (SEQ ID NO: 46), G96956 (SEQ ID NO: 47), H82630 (SEQ ID NO: 48), Q83EP5 (SEQ ID NO: 49), Q87CN3 (SEQ ID NO: 50), Q87HT6 (SEQ ID NO: 51), Q87QB9 (SEQ ID NO: 52), ZP00033810 (SEQ ID NO: 53), ZP00064975 (SEQ ID NO: 54), ZP00116993 (SEQ ID NO: 55)) and the corresponding conserved amino acid residues. Conserved residues are shaded in grey. The consensus for these residues is given below the sequences: capital letters denote mandatory residues; regular letters give the most prominent amino acid of a mandatory similarity group at this location.

In the specification at page 49 line 21, please replace the paragraph starting with "peptide 1" with the following amended paragraph:

peptide 1 ACLKPLGATYTNR (SEQ ID NO: 14)

peptide 2 AALEAGLYAR (SEQ ID NO: 15)

peptide 3 VLVLGCSTGYGLSTR (SEQ ID NO: 16)

peptide 4 TDPAT (SEQ ID NO: 17)

peptide 5 SLDGDAFDSTTK (SEQ ID NO: 18)

peptide 6 DLWSQVNTANLK (SEQ ID NO: 19)

peptide 7 AGWYNTVAFEK (SEQ ID NO: 20)

peptide 8 RVQEELAYAR (SEQ ID NO: 21)

peptide 9 DLSDFAGYQTEFLR (SEQ ID NO: 22)

peptide 10 LYPGDGSPLVDEAGR (SEQ ID NO: 23)

peptide 11 LTQQYGCPAYPVVAK (SEQ ID NO: 24)

In the specification at page 50 line 1, please replace the paragraph starting with "peptide 12" with the following amended paragraph:

peptide 12 VDDWEMAEDVQQAVK (SEQ ID NO: 25)

peptide 13 STGYG(AMVR/LSEK) (SEQ ID NO: 26)

peptide 14 AHPPTSPGPK (SEQ ID NO: 27)

peptide 15 ALSEAGVLAEQK (SEQ ID NO: 28)

peptide 16 ((GT)/(AS))HEGCLEQMVR (SEQ ID NO: 29)

peptide 17 LYPENGAPLVDEQR (SEQ ID NO: 30)

Degenerate primers were designed according to these peptides and used for PCR with cDNA as template. Due to the high GC-content of *E. gracilis* an initial denaturation of 98°C for 10 min was accomplished prior to PCR. PCR conditions were as follows: 30 cycles with 94°C for 30 sec; 50°C for 30 sec and 72°C for 90 sec; final extension at 72°C for 5 min. A 837 bp fragment was amplified with the following primers: 5'-GGITGGTAYAAYACIGTIGC-3' (SEQ ID NO: 12) (referring to peptide 7) and 5'-GTYTCRTAICCIGCRAARTC-3' (SEQ ID NO: 13) (referring to peptide 9). This fragment was cloned into pBluescript SK+/HincII and sequenced (SEQ ID NO : 3). The translated sequence contained several peptides of the purified protein and therefore the 837 bp

fragment was used as hybridisation probe to screen a cDNA library constructed with mRNA from aerobically grown *Euglena* cells as described in example 2 and 3. Screening of 250.000 recombinant phages resulted in six independent clones. cDNA inserts varied between 1600 bp and 1900 bp. Sequencing of all six clones from both ends revealed that all clones represented the same transcript and varied only in length. The longest clone was sequenced completely double-stranded via deletion by exonuclease III. The clone had a length of 1912 bp and encodes an open reading frame of 1620 bp coding for 539 aa (SEQ ID NO : 1 and SEQ ID NO : 2). At both ends it had adaptors consisting of a NotI and EcoRI restriction site and was inserted into the EcoRI site of the vector pBluescript SKP. Figure 3 shows the map of the TER clone in the vector pBluescript SKP.

In the specification at page 52 line 4, please replace the paragraph starting with "TER1Ndefor" with the following amended paragraph:

TER1Ndefor 5'-TAT ACA TAT GTC GTG CCC CGC CTC GCC GTC TG-3' (SEQ ID NO: 31) *Nde* I

TER1Bglfor 5'-TAT AGA TCT TAT GTC GTG CCC CGC CTC GCC GTC TG-3' (SEQ ID NO: 32) *Bgl* II

TER2Ndefor 5'-TAT ACA TAT GTT CAC CAC CAC AGC GAA GGT CAT CC-3' (SEQ ID NO: 33) *Nde* I

TERXhorev 5'-TAT CTC GAG CTA CTG CTG GGC AGC ACT GG-3' (SEQ ID NO: 34) *Xho* I